

IN THE SPECIFICATIONS:

Please amend the specifications as follows (amendments are underlined):

The paragraph bridging pages 5–6 of the instant specification:

Computer-assisted analysis suggests that mature IL-17RLM-L contains a putative signal peptide of 16 amino acids, a 281-amino acid extracellular domain (C17-Pro297), a 23-amino acid transmembrane stretch (Ile298-Met320), and a 420-amino acid longer cytoplasmic tail (Cys321-Leu739) than that of IL-17BR/IL-17Rh1. The cytoplasmic portion of this new receptor polypeptide of the invention is much longer than IL-17BR, and is comparable with the unusually long tail described for IL-17 receptor. Additionally, there are nine cystine residues in extracellular domain and eight potential N-linked glycosylation sites in the extracellular domain of the polypeptide of the invention. The extracellular domain also consists of a predicted immunoglobulin domain and a putative fibronectin III domain. This protein is predicted to be a type I membrane protein according to Hartmann membrane topology model and PSORT II server prediction. But there is no WSXWS (SEQ ID NO:20) motif, typical of type I receptor (32,33) in the extracellular domain. The sequence of IL-17RLM-L is slightly atypical for type I cytokine receptors in that the usual WSXWS (SEQ ID NO:20) motif is replaced by WSPGA (SEQ ID NO:21). Furthermore, a segment (TPPPLRPRKVW (SEQ ID NO:22)) located proximal to the IL-17 receptor transmembrane domain, which is highly conserved among cytokine receptor, is replaced by the proline-rich motif (PFHPPPLRYREP (SEQ ID NO:23)), which was a typical feature of a transactivation domain for transcription factors. Interestingly, both a putative TIR domain (Toll/IL-1-Receptor homology domain) and a putative SH3 interaction domain (proline-rich domain) were predicted in the intracellular domain of the protein from (V358 to K424). Additionally, a putative tyrosine phosphorylation site juxtaposed to the transmembrane domain (Y329) was also identified. The long COOH-terminal tail (C-tail) of IL-17RLM also contains multiple tyrosine residues and putative Stat binding motifs.

At page 10, 3rd paragraph of the instant specification:

Electrophoretic mobility-shift assay DNA probes [double-stranded β -casein promoter GAS (γ -interferon activated sequence): 5'-AGATTCTAGGAATTC-3' (SEQ ID NO:19)] were prepared by end-labeling with [γ -³²P]ATP and T4 polynucleotide kinase and purified by G-50 MicroSpin columns. Cells were washed three times in PBS and starved in the absence of cytokines for 8 hrs in RPMI 1640. Cells were then stimulated for the indicated times with the indicated cytokine at a concentration used in growth medium. Typically, 5 μ l (10-20 μ g) of nuclear proteins was incubated with 100,000 cpm of ³²P-labeled oligonucleotides for 2 hrs at room temperature. The nuclear proteins and various oligonucleotide probes were incubated in buffer containing 10 mM Tris (pH 7.5), 10% glycerol, and 0.2% Nonidet P-40. Additionally, 2-4 μ g of poly (dI-dC) was included as a nonspecific competitor DNA. Protein-DNA complexes were resolved on 4% nondenaturing polyacrylamide gels in 0.5 \times TBE running buffer. After electrophoresis, gels were dried and subjected to autoradiography. Antibody supershift experiments were carried out by addition of 4 μ l of various antibodies purchased from Santa Cruz Biotechnology.

At page 13, 1st paragraph of the instant specification:

Computer-assisted analysis suggested that hIL-17RLM-L contained a putative signal peptide of 16 amino acids, a 281-amino acid extracellular domain (C¹⁷-Pro²⁹⁷), a 23-amino acid transmembrane stretch (Ile²⁹⁸-Met³²⁰), and a 420-amino acid cytoplasmic tail (Cys³²¹-Leu⁷³⁹). The cytoplasmic portion of this new receptor was much longer than that of IL-17BR, and comparable with the unusually long tail of IL-17AR. This protein was predicted to be a type I cytokine receptor according to Hartmann membrane topology model and PSORT II server. However, hIL-17RLM-L had a WSPGA (SEQ ID NO:21) instead of WSXWS (SEQ ID NO:20) motif, which is a typical motif in the extracellular domain of type I cytokine receptors (33, 34). There were eight cystine residues and nine potential N-linked glycosylation sites in the extracellular domain, where an immunoglobulin domain and a fibronectin III domain were also predicted. Furthermore, a highly cytokine receptor conserved segment (TPPPLRPRKVW (SEQ ID NO:22)) located proximal to the IL-17

receptor transmembrane domain was replaced by the proline-rich segment (PFHPPPLRYREP (SEQ ID NO:23)), a putative SH3 interaction domain, which was a typical feature of a transactivation domain for transcription factors. Additionally, a putative TIR domain (V³⁵⁸ to K⁴²⁴) (Toll/IL-1Receptor domain) and a putative TRAF6 binding motif (P³⁴⁷ to L³⁵¹), Pro-X-Glu-X-X (aromatic/acidic residue) were predicted in the intracellular portion of hIL-17RLM-L. The TRAF6 binding motif was found in TRANCE-R and IRAK adapter kinases for ILR/Toll-like receptor signaling(35), suggesting that hIL-17RLM may play a role in the Toll-like receptor signaling. The long COOH-terminal tail (C-tail) of hIL-17RLM also contained multiple tyrosine residues. All of these implied that the protein might be a novel signaling receptor.

Please **delete** the prior “SEQUENCE LISTING” and **replace** it with the following revised SEQUENCE LISTING (changes relative to the previous version are underlined):

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35 40 45

Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser
50 55 60

Gln His Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn
65 70 75 80

Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly
85 90 95

Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Met Thr
100 105 110

Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu
115 120 125

Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys
130 135 140

Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr
145 150 155 160

Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met
165 170 175

Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu
180 185 190

Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu
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Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln
210 215 220

Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe
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Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys
245 250 255

Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln
260 265 270

Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys
275 280 285

Lys Asn Tyr Lys His Lys Gly Gly Arg Gly Ser Gly Lys Gly Glu
290 295 300

Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala
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Lys Gln Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe
325 330 335

Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr
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Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His
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Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly
370 375 380

Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val
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Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe
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Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu
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Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met
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Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala
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Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His
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Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser
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Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser
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Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser
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Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu
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Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Gly Leu Gly Glu
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